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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2009; month=10; day=5; hr=15; min=8; sec=12; ms=280;]

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Application No: 10550363 Version No: 2.0

Input Set:

Output Set:

Started: 2009-09-18 16:25:00.198
Finished: 2009-09-18 16:25:01.941
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 743 ms
Total Warnings: 13
Total Errors: 0
No. of SeqIDs Defined: 20
Actual SeqID Count: 20

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
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W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

SEQUENCE LISTING

<110> Glaxo Group Limited
 VINSON, Mary
 IRVING, Elaine Alison

<120> THERAPEUTICAL USE OF ANTI-MYELIN
 ASSOCIATED GLYCOPROTEIN (MAG) ANTIBODIES

<130> PB60024

<140> 10550363
 <141> 2009-09-18

<150> PCT/EP2004/001016
 <151> 2004-02-02

<150> 0306309.6
 <151> 2003-03-19

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1
 <211> 17
 <212> PRT
 <213> MUS MUSCULUS

<400> 1
 Lys Ser Ser His Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu
 1 5 10 15
 Ala

<210> 2
 <211> 7
 <212> PRT
 <213> MUS MUSCULUS

<400> 2
 Trp Ala Ser Thr Arg Glu Ser
 1 5

<210> 3
 <211> 8
 <212> PRT
 <213> MUS MUSCULUS

<400> 3
 His Gln Tyr Leu Ser Ser Leu Thr
 1 5

<210> 4
<211> 5
<212> PRT
<213> MUS MUSCULUS

<400> 4
Asn Tyr Gly Met Asn
1 5

<210> 5
<211> 17
<212> PRT
<213> MUS MUSCULUS

<400> 5
Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Thr
1 5 10 15
Gly

<210> 6
<211> 17
<212> PRT
<213> MUS MUSCULUS

<400> 6
Asn Pro Ile Asn Tyr Tyr Gly Ile Asn Tyr Glu Gly Tyr Val Met Asp
1 5 10 15
Tyr

<210> 7
<211> 475
<212> PRT
<213> MUS MUSCULUS

<400> 7
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15
Val His Ser Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
20 25 30
Pro Gly Glu Thr Asn Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
50 55 60
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
65 70 75 80
Asp Asp Phe Thr Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
85 90 95
Thr Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asn Glu Asp Thr Ala Thr
100 105 110
Tyr Phe Cys Ala Arg Asn Pro Ile Asn Tyr Tyr Gly Ile Asn Tyr Glu

115	120	125
Gly Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser		
130	135	140
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser		
145	150	155
Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp		
165	170	175
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr		
180	185	190
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr		
195	200	205
Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln		
210	215	220
Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp		
225	230	235
Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro		
245	250	255
Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu Phe Pro		
260	265	270
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr		
275	280	285
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn		
290	295	300
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg		
305	310	315
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val		
325	330	335
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser		
340	345	350
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys		
355	360	365
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp		
370	375	380
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe		
385	390	395
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu		
405	410	415
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe		
420	425	430
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly		
435	440	445
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr		
450	455	460
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
465	470	475

<210> 8

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain

<400> 8

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1	5	10	15
Val His Ser Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala Val			
20	25	30	
Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser His Ser Val			
35	40	45	
Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys			
50	55	60	
Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu			
65	70	75	80
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe			
85	90	95	
Thr Leu Thr Ile Ile Asn Val His Thr Glu Asp Leu Ala Val Tyr Tyr			
100	105	110	
Cys His Gln Tyr Leu Ser Ser Leu Thr Phe Gly Thr Gly Thr Lys Leu			
115	120	125	
Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro			
130	135	140	
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu			
145	150	155	160
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn			
165	170	175	
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser			
180	185	190	
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala			
195	200	205	
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly			
210	215	220	
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
225	230	235	

<210> 9

<211> 475

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 9

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly			
1	5	10	15
Val His Ser Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys			
20	25	30	
Pro Gly Glu Thr Asn Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe			
35	40	45	
Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu			
50	55	60	
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala			
65	70	75	80
Asp Asp Phe Thr Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser			
85	90	95	
Thr Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asn Glu Asp Thr Ala Thr			
100	105	110	
Tyr Phe Cys Ala Arg Asn Pro Ile Asn Tyr Tyr Gly Ile Asn Tyr Glu			
115	120	125	
Gly Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser			

130		135		140	
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser					
145		150		155	160
Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp					
	165		170		175
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr					
	180		185		190
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr					
	195		200		205
Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln					
	210		215		220
Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp					
225		230		235	240
Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro					
	245		250		255
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro					
	260		265		270
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr					
	275		280		285
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn					
	290		295		300
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg					
305		310		315	320
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val					
	325		330		335
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser					
	340		345		350
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys					
	355		360		365
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp					
	370		375		380
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe					
385		390		395	400
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu					
	405		410		415
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe					
	420		425		430
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly					
	435		440		445
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr					
	450		455		460
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys					
465		470		475	

<210> 10

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain variable region

<400> 10

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala			
1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr			

Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	Ala	Asp	Asp	Phe
50						55					60				
Thr	Gly	Arg	Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Tyr
65					70					75					80
Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys
				85					90					95	
Ala	Arg	Asn	Pro	Ile	Asn	Tyr	Tyr	Gly	Ile	Asn	Tyr	Glu	Gly	Tyr	Val
			100					105					110		
Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
		115					120						125		

<210> 13
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Heavy chain variable region

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ser	Glu	Leu	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Asn	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
			20					25					30		
Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	Ala	Asp	Asp	Phe
50						55					60				
Thr	Gly	Arg	Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Tyr
65					70					75					80
Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys
				85					90					95	
Ala	Arg	Asn	Pro	Ile	Asn	Tyr	Tyr	Gly	Ile	Asn	Tyr	Glu	Gly	Tyr	Val
			100					105					110		
Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
		115					120						125		

<210> 14
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain variable region

Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	His	Ser	Val	Leu	Tyr	Ser
			20						25				30		
Ser	Asn	Gln	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln
		35					40					45			
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val
50					55						60				
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr

65		70		75		80									
Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	His	Gln
			85						90					95	
Tyr	Leu	Ser	Ser	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100					105					110		
Arg	Thr	Val													
		115													

<210> 15

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain variable region

<400> 15

Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly
1				5				10					15		
Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	His	Ser	Val	Leu	Tyr	Ser
			20					25					30		
Ser	Asn	Gln	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln
		35					40					45			
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val
		50				55					60				
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
65				70						75					